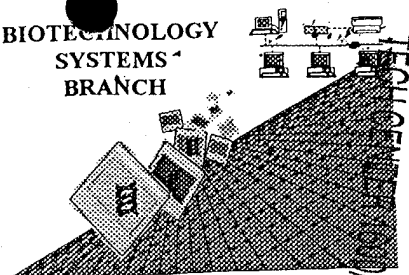


555

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



OCT 05 2001

#10  
RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/550,605  
Source: O.I.P.E.  
Date Processed by STIC: 08/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/550,605

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos    was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
                          prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering               use space characters, instead.
  
- 4      Non-ASCII            The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
                          ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
                          each n or Xaa can only represent a single residue. Please present the maximum number of each  
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0        A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"                   sequences(s)     . Normally, PatentIn would automatically generate this section from the  
                          previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
                          the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
                          Artificial or Unknown sequences.
  
- 7      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                          (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                          This sequence is intentionally skipped  
  
                          Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)            <210> sequence id number  
                          <400> sequence id number  
                          000
  
- 9      Use of n's or Xaa's    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)            Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                          In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>        Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response               scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
                          is Artificial Sequence
  
- 11    ☒ Use of <220>            Sequence(s)   5   missing the <220> "Feature" and associated numeric identifiers and responses.  
                          Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
                          "Unknown." Please explain source of genetic material in <220> to <223> section.  
                          (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0        Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"                   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence  
                          listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/550,605

DATE: 08/23/2001

TIME: 11:26:59

Input Set : A:\p20434us-m.txt

Output Set: N:\CRF3\08162001\I550605.raw

5 <110> APPLICANT: Melica HB  
 7       Andersson, Leif  
 9       Marklund, Stefan  
 11       Kijas, James  
 13       Moller, Maria  
 15       Wales, Richard  
 19 <120> TITLE OF INVENTION: Methods for determining Coat colour genotypes in pigs  
 23 <130> FILE REFERENCE: 064727.0109  
 C--> 27 <140> CURRENT APPLICATION NUMBER: US/09/550,605  
 29 <141> CURRENT FILING DATE: 2000-04-17  
 33 <150> PRIOR APPLICATION NUMBER: GB 9722027.1  
 35 <151> PRIOR FILING DATE: 1997-10-17  
 39 <150> PRIOR APPLICATION NUMBER: PCT/GB98/03081  
 41 <151> PRIOR FILING DATE: 1998-10-13  
 45 <160> NUMBER OF SEQ ID NOS: 11  
 49 <170> SOFTWARE: PatentIn version 3.1  
 53 <210> SEQ ID NO: 1  
 55 <211> LENGTH: 22  
 57 <212> TYPE: DNA  
 59 <213> ORGANISM: Artificial sequence  
 63 <220> FEATURE:  
 65 <223> OTHER INFORMATION: Primer  
 67 <400> SEQUENCE: 1  
 68 gtattcacag agacttggcg gc 22  
 71 <210> SEQ ID NO: 2  
 73 <211> LENGTH: 24  
 75 <212> TYPE: DNA  
 77 <213> ORGANISM: Artificial sequence  
 81 <220> FEATURE:  
 83 <223> OTHER INFORMATION: Primer  
 85 <400> SEQUENCE: 2  
 86 aaacctgcaa ggaaaatcct tcac 24  
 89 <210> SEQ ID NO: 3  
 91 <211> LENGTH: 25  
 93 <212> TYPE: DNA  
 95 <213> ORGANISM: Artificial sequence  
 99 <220> FEATURE:  
 101 <223> OTHER INFORMATION: Primer  
 103 <400> SEQUENCE: 3  
 104 tcrtacatag aaagagaygt gactc 25  
 107 <210> SEQ ID NO: 4  
 109 <211> LENGTH: 23  
 111 <212> TYPE: DNA  
 113 <213> ORGANISM: Artificial sequence  
 117 <220> FEATURE:  
 119 <223> OTHER INFORMATION: Primer  
 121 <400> SEQUENCE: 4

Does Not Comply  
Corrected Diskette Needed

See page 2 of 5

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/550,605

DATE: 08/23/2001

TIME: 11:26:59

Input Set : A:\p20434us-m.txt

Output Set: N:\CRF3\08162001\I550605.raw

122 agccttcctt gatcatcttg tag 23

125 <210> SEQ ID NO: 5

127 <211> LENGTH: 26

129 <212> TYPE: DNA

C--> 131 <213> ORGANISM: Artificial

W--> 135 <220> FEATURE:

W--> 135 <223> OTHER INFORMATION:                      Errored The 213 response

135 <400> SEQUENCE: 5 "Artificial", "Artificial Sequence" or

136 aaacctgcaa ggaaatcct tcacgg "Unknown" requires an explanation

139 <210> SEQ ID NO: 6 or description in field 223

141 <211> LENGTH: 24

143 <212> TYPE: DNA

145 <213> ORGANISM: Artificial sequence

149 <220> FEATURE:

151 <223> OTHER INFORMATION: Primer OK

153 <400> SEQUENCE: 6

154 ctcttactc atggtcgaat caca 24

157 <210> SEQ ID NO: 7

159 <211> LENGTH: 21

161 <212> TYPE: DNA

163 <213> ORGANISM: Artificial sequence

167 <220> FEATURE:

169 <223> OTHER INFORMATION: Primer

171 <400> SEQUENCE: 7

172 cggctaaaat gcatggtatg g 21

175 <210> SEQ ID NO: 8

177 <211> LENGTH: 27

179 <212> TYPE: DNA

181 <213> ORGANISM: Artificial sequence

185 <220> FEATURE:

187 <223> OTHER INFORMATION: Primer

189 <400> SEQUENCE: 8

190 tcaaaggaaa catgagtacc cacgctc 27

193 <210> SEQ ID NO: 9

195 <211> LENGTH: 25

197 <212> TYPE: DNA

199 <213> ORGANISM: Artificial sequence

203 <220> FEATURE:

205 <223> OTHER INFORMATION: Primer

207 <400> SEQUENCE: 9

208 tcaaaggaaa cgtgagtacc cacgc 25

211 <210> SEQ ID NO: 10

213 <211> LENGTH: 48

215 <212> TYPE: DNA

217 <213> ORGANISM: Sus scrofa

221 <400> SEQUENCE: 10

222 aattacgtgg tcaaaggaaa cgtgagtacc cacgctctcc tgacagtc 48

225 <210> SEQ ID NO: 11

227 <211> LENGTH: 48

RAW SEQUENCE LISTING

DATE: 08/23/2001

PATENT APPLICATION: US/09/550,605

TIME: 11:26:59

Input Set : A:\p20434us-m.txt

Output Set: N:\CRF3\08162001\I550605.raw

229 <212> TYPE: DNA

231 <213> ORGANISM: Sus scrofa

235 <400> SEQUENCE: 11

236 aattacgtgg tcaaaggaaa catgagtacc cacgctctcc tgacagtc

48

**STATISTICS SUMMARY**

PATENT APPLICATION: US/09/550,605

DATE: 08/23/2001

TIME: 11:27:00

Input Set : A:\p20434us-m.txt

Output Set: N:\CRF3\08162001\I550605.raw

Application Serial Number: US/09/550,605

Alpha or Numeric: Numeric

Application Class:

Application File Date: 04-17-2000

Art Unit: OIPE

Software Application: PatentIn

Total Number of Sequences: 11

Total Nucleotides: 313

Total Amino Acids: 0

Number of Errors: 0

Number of Warnings: 2

Number of Corrections: 2

**MESSAGE SUMMARY**

220 C: 1 (Keyword misspelled or invalid format)

258 W: 2 (Mandatory Feature missing)

270 C: 1 (Current Application Number differs)